



<110> Maxygen ApS Maxygen Holdings Ltd.

Single-Chain Polypeptides <120>

<130> 0218us210

<150> US 60/245,727

<151> 2000-11-02

<160> 16

PatentIn version 3.1 <170>

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<211> 174

<212> **PRT**

<213> Homo sapiens

<400>

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys $1 \hspace{1cm} 5 \hspace{1cm} 10 \hspace{1cm} 15$

Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln 20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys $50 \hspace{1.5cm} 55 \hspace{1.5cm} 60$

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser 85 90 95
Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp 100 105 110
Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro 115 120 125
Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe 130 135 140
Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe 145 150 155 160
Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro 165 170
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<213> Saccharomyces cerevisiae
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ggt 63
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<220>
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atggcc	126
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ttgtgtcatc cagaagaatt ggttttgttg ggtcattctt tgggtattcc atg	ggctcca 180
ttgtcttctt gtccatctca agctttgcaa ttggctggtt gtttgtctca att	gcattct 240
ggtttgtttt tgtatcaagg tttgttgcaa gctttggaag gtatttctcc aga	attgggt 300
ccaactttgg atactttgca attggatgtt gctgattttg ctactactat ttg	gcaacaa 360
atggaagaat tgggtatggc tccagctttg caaccaactc aaggtgctat gcc	agctttt 420
gcttctgctt ttcaaagaag agctggtggt gttttggttg cttctcattt gca	atctttt 480
ttggaagttt cttatagagt tttgagacat ttggctcaac ca	522
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ctgtgccatc ctgaagaact ggtcctgtta ggccatagct taggcatccc gtg	ggcgcct 180
ctgagtaget georgagtea ggeetgeag etggeegget geotgagtea gtt	acatagt 240

ggcttatttt tatatcaggg cttactgcag gcgttagaag gcattagtcc ggaactgggc 300 ccgaccctgg ataccttaca gttagatgtc gcggattttg ccaccaccat ttggcagcag 360 atggaagaat taggcatggc gcctgcgtta cagcctaccc agggcgccat gcctgcgttt 420 gcgagtgcgt ttcagcgtcg cgccggcggc gtgttagtgg ccagccatct gcagagcttt 480 ctggaagtga gttatcgtgt gttacgccat ctggcccagc cttaatctag a 531

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Cys Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
20 25 30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val 35 40 45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys 50 60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser 65 70 75 80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser 85 90 95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp 100 105 110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro 115 120 125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe 130 135 140 Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe 145 150 155 160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Thr Pro 165 170 175

Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu 180 185 190

Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln Glu Lys 195 200 205

Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val Leu Leu 210 215 220

Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys Pro Ser 225 230 235 240

Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser Gly Leu 245 250 255

Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser Pro Glu 260 265 270

Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp Phe Ala 275 280 285

Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro Ala Leu 290 295 300

Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe Gln Arg 305 310 315 320

Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe Leu Glu 325 330 335

Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro 340 345

<210> 7

<211> 90

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<213> Homo sapiens

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<212> DNA
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                                                                     120
ttgtgtcatc cagaagaatt ggttttgttg ggtcattctt tgggtattcc atgggctcca
                                                                     180
ttgtcttctt gtccatctca agctttgcaa ttggctggtt gtttgtctca attgcattct
                                                                     240
ggtttgtttt tgtatcaagg tttgttgcaa gctttggaag gtatttctcc agaattgggt
                                                                     300
ccaactttgg atactttgca attggatgtt gctgattttg ctactactat ttggcaacaa
                                                                     360
atggaagaat tgggtatggc tccagctttg caaccaactc aaggtgctat gccagctttt
                                                                     420
gcttctgctt ttcaaagaag agctggtggt gttttggttg cttctcattt gcaatctttt
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His His His His His
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  <211>
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Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
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